

SEQUENCE LISTING

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<220>

<223> Primer

<120> ESCHERICHIA COLI STRAIN SECRETING HUMAN
 GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)

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<130> HYLEE60.001APC
<140> US 10/009,792
<141> 2001-11-13
<150> PCT/KR01/00549
<151> 2001-03-31
<150> KR 10-2000-0017052
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agetteetge teaagtgett agageaagtg aggaagatee agggegatgg egeagegete 180
caggagaagc tggcaggctg cttgagccaa ctccatagcg gccttttcct ctaccagggg 240
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ctggacgtcg ccgactttgc caccaccatc tggcagcaga tggaagaact gggaatggcc 360
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gcaggagggg tcctagttgc ctcccatctg cagagcttcc tggaggtgtc gtaccgcgtt 480
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gcaggetget tgagecaact ccatagegge etttteetet accagggget cetgcaggee 360
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gactttgcca ccaccatctg gcagcagatg gaagaactgg gaatggcccc tgccctgcag 480
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                 5
Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
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                                25
Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
                                               45
                            40
Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
                        55
                                            60
Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
                    70
                                        75
Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                85
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
                                105
                                                    110
            100
Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
                                                125
Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
                        135
                                            140
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
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Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
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aagctgtgcc accccgagga gctggtgctg ctcggacact ctctgggcat cccctgggct 180
cccctgagca gctgccccag ccaggccctg cagctggcag gctgcttgag ccaactccat 240
ageggeettt teetetacea ggggeteetg eaggeeetgg aagggatete eeeegagttg 300
ggtcccacct tggacacact gcagctggac gtcgccgact ttgccaccac catctggcag 360
cagatggaag aactgggaat ggcccctgcc ctgcagccca cccagggtgc catgccggcc 420
ttcgcctctg ctttccagcg ccgggcagga ggggtcctag ttgcctccca tctgcagagc 480
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<210> 21

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           5
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        20
                              25
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
                           40
Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
                       55
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
                   7.0
Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                                   90
               8.5
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
           100
                              105
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
    115
                           120
Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
                       135
Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
                   150
                                      155
Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                                170
               165
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Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu
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ttcctgctca agtgc

135

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        20
                               25
Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys
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aggacteegt taggteeage eageteeetg ecceagaget teetgeteaa gtgettagag 180
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Met Ser Ile Ser Met Phe Ser Ala Thr Ala Ser Ala Ala Gly Pro His
        20
                               25
His His His His Ile Glu Gly Arg Thr Pro Leu Gly Pro Ala Ser
                           40
Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu
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30

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